SPE RESPONSE FOR CERTIFICATE OF CORRECTION

Paper No.: _____

DATE : 4/5/06

TO SPE OF : ART UNIT 1656

SUBJECT : Request for Certificate of Correction for Appl. No.: 09/832929 Patent No.: 6926898

Please respond to this request for a certificate of correction within 7 days.

Please review the requested changes/corrections as shown in the COCIN document(s) in the IFW application image. No new matter should be introduced, nor should the scope or meaning of the claims be changed.

Please complete the response (see below) and forward the completed response to scanning using document code **COCX**.

Certificates of Correction Branch

703-308-9390 ext. _____

Thank You For Your Assistance

The request for issuing the above-identified correction(s) is hereby:

Note your decision on the appropriate box.

☒ Approved	All changes apply.
☐ Approved in Part	Specify below which changes **do not** apply.
☐ Denied	State the reasons for denial below.

Comments: _____

KATHLEEN M. KERR, PH.D.
SUPERVISORY PATENT EXAMINER

SPE

1656
Art Unit

UNITED STATES PATENT AND TRADEMARK OFFICE

CERTIFICATE OF CORRECTION

PATENT NO. 6,926,898

APPLICATION NO.: 09/832,929

ISSUE DATE: August 9, 2005

INVENTOR(S): Craig A. Rosen and William A. Haseltine

It is hereby certified that an error or errors appear in the above-identified patent and that said Letters Patent is hereby corrected as shown below:

Under item (60) (Related U.S. Application Data) of the title page, delete the text beginning with "Provisional application No. 60/256,931" to and ending "provisional application No. 60/229,358, filed on Apr. 12, 2000."

Under item (56) (References Cited) of the title page and under U.S. PATENT DOCUMENTS beginning on page 1, insert:

--	2003-0022308 A1	1/2003	Fleer et al.
	2003-0036170 A1	2/2003	Fleer et al.
	2003-0036171 A1	2/2003	Fleer et al.
	2003-0036172 A1	2/2003	Fleer et al.
	2003-0054554 A1	3/2003	Becquart et al.
	2003-0082747 A1	5/2003	Fleer et al.
	2003-0104578 A1	10/2001	Ballance
	2004-0010134 A1	4/2001	Rosen et al.
	09/832,501	4/2001	Ballance et al.
	09/833,041	4/2001	Rosen et al.
	09/833,111	4/2001	Rosen et al.
	09/833,117	4/2001	Rosen et al.
	09/833,118	4/2001	Rosen et al.
	10/702,536	11/2003	Fleer et al.
	10/702,636	11/2003	Fleer et al. --

MAILING ADDRESS OF SENDER

Finnegan, Henderson, Farabow,
Garrett & Dunner, L.L.P.
901 New York Avenue, N.W.
Washington, D.C. 20001-4413

Under item (56) (References Cited) of the title page and under OTHER PUBLICATIONS beginning on page 1, insert:

-- Larsson, M., et al., "Role of Annexins in Endocytosis of Antigens in Immature Human Dendritic Cells," *Immunology* 92:501-511 (1997).

Latta, M. et al., "Synthesis and Purification of Mature Human Serum Albumin From *E. Coli*," *Bio/Technology* 5:1309-1314 (1987).

Latta, M., et al., "Tryptophan Promoter Derivatives on Multicopy Plasmids: A Comparative Analysis of Expression Potentials in *Escherichia coli*," *DNA and Cell Biology* 9:129-137 (1990).

Lawn, R.M., et al., "The Sequence of Human Serum Albumin cDNA and its Expression in E. coli," *Nucleic Acids Research* 9:6103-6113 (1981).

Le Bras, M., et al., " Epidemiologie et Clinique des Maladies Tropicales D'importation," *La Revue de Medicine Interne* 13:205-210 (1992), with English translation.

Leblois, H., et al., "Stable Transduction of Actively Dividing Cells via a Novel Adenoviral/Episomal Vector," *Molecular Therapy* 1:314-322 (2000).

Lee, C-H., et al., "Sodium Pertechnetate Tc99m Antral Scan in the Diagnosis of Retained Gastric Antrum," *Arch. Surg.* 119: 309-311 (1984).

Lee, C-L., et al., "Preparation and Characterization of Polyethylene-Glycol-Modified Salmon Calcitonins," *Pharmaceutical Development and Technology,* 4(2): 269-275 (1999).

Lee, W-C., et al., "Identification and Characterization of a Nuclear Localization Sequence-Binding Protein in Yeast," *Proc. Natl. Acad. Sci. USA* 86:8808-8812 (1989).

Lee, Y-H., et al., "Comparison of Effective Renal Plasma Flow (ERPF) and Endogenous Creatinine Clearance (Ccr) in Evaluation of the Differential Kidney Function: An in Vivo Study," *Chin. Med. J. (Taipei)* 49:147-152 (1992).

Lei, H-Y., et al., "An Antigen-specific Hypersensitivity Which Does Not Fit Into Traditional Classification of Hypersensitivity," *The Journal of Immunology* 143:432-438 (1989).

Levitt, D., et al., "Toxicity of Perfluorinated Fatty-Acids for Human and Murine B Cell Lines," *Toxicology and Applied Pharmacology* 86:1-11 (1986).

Finnegan, Henderson, Farabow,
Garrett & Dunner, L.L.P.
901 New York Avenue, N.W.
Washington, D.C. 20001-4413

Lew D.B., et al., "Mitogenic Effect of Lysosomal Hydrolases on Bovine Tracheal Myocytes in Culture," *The Journal of Clinical Investigation* 88:1969-1975 (1991).

Lewis, C., et al., "Is Sexual Dysfunctoin in Hypertensive Women Uncommon or Understudied?" *American Jour of Hypertension*," 11:733-735 (1998). --

Under item (57) (ABSTRACT) of the title page, "disordrs" should read --disorders--.

In the Specification

Col. 143, line 26, delete "As exhibited in Table 2, most", and insert --Most--.

Col. 143, line 31, delete "Table 2".

In the Claims

Col. 340, line 40, delete "an".

Col. 340, line 47, delete "an".

In the Sequence Listing

Delete the Sequence Listing beginning in Col. 299, beginning with the text "<160> NUMBER OF SEQ ID NOS: 72" to and ending "<400> SEQUENCE: 72

```
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
   1               5                  10                  15"
```

in Col. 340 and insert the following Sequence Listing:

```
<160> NUMBER OF SEQ ID NOS: 82

<210> 1
<211> 23
<212> DNA
<213> Artificial Sequence
<220>
<221> primer_bind
<223> primer useful to clone human growth hormone cDNA

<400> 1
cccaagaatt cccttatcca ggc                                          23

<210> 2
<211> 33
<212> DNA
<213> Artificial Sequence
<220>
<221> primer_bind
```

<223> primer useful to clone human growth hormone cDNA

<400> 2
gggaagctta gaagccacag gatccctcca cag 33

<210> 3
<211> 16
<212> DNA
<213> Artificial Sequence
<220>
<221> misc_structure
<223> synthetic oligonucleotide used to join DNA fragments with non-cohesive ends.

<400> 3
gataaagatt cccaac 16

<210> 4
<211> 17
<212> DNA
<213> Artificial Sequence
<220>
<221> misc_structure
<223> synthetic oligonucleotide used to join DNA fragments with non-cohesive ends.

<400> 4
aattgttggg aatcttt 17

<210> 5
<211> 17
<212> DNA
<213> Artificial Sequence
<220>
<221> misc_structure
<223> synthetic oligonucleotide used to join DNA fragments with non-cohesive ends.

<400> 5
ttaggcttat tcccaac 17

<210> 6
<211> 18
<212> DNA
<213> Artificial Sequence
<220>
<221> misc_structure
<223> synthetic oligonucleotide used to join DNA fragments with non-cohesive ends.

<400> 6
aattgttggg aataagcc 18

<210> 7
<211> 24
<212> PRT
<213> Artificial Sequence
<220>
<221> SITE
<222> 1)..(19)
<223> invertase leader sequence
<220>
<221> SITE
<222> 20)..(24)
<223> first 5 amino acids of mature human serum albumin

<400> 7
Met Leu Leu Gln Ala Phe Leu Phe Leu Leu Ala Gly Phe Ala Ala Lys
1 5 10 15

Ile Ser Ala Asp Ala His Lys Ser
20

<210> 8
<211> 21
<212> DNA
<213> Artificial Sequence
<220>
<221> misc_structure
<223> synthetic oligonucleotide used to join DNA fragments with non-cohesive ends.

<400> 8
gagatgcaca cctgagtgag g 21

<210> 9
<211> 27
<212> DNA
<213> Artificial Sequence
<220>
<221> misc_structure
<223> synthetic oligonucleotide used to join DNA fragments with non-cohesive ends.

<400> 9
gatcctgtgg cttcgatgca cacaaga 27

<210> 10
<211> 24
<212> DNA
<213> Artificial Sequence
<220>
<221> misc_structure
<223> synthetic oligonucleotide used to join DNA fragments with non-cohesive ends.

<400> 10
ctcttgtgtg catcgaagcc acag 24

<210> 11
<211> 30
<212> DNA
<213> Artificial Sequence
<220>
<221> misc_structure
<223> synthetic oligonucleotide used to join DNA fragments with non-cohesive ends.

<400> 11
tgtggaagag cctcagaatt tattcccaac 30

<210> 12
<211> 31
<212> DNA
<213> Artificial Sequence
<220>
<221> misc_structure
<223> synthetic oligonucleotide used to join DNA fragments with non-cohesive ends.

<400> 12
aattgttggg aataaattct gaggctcttc c 31

<210> 13
<211> 47
<212> DNA
<213> Artificial Sequence
<220>
<221> misc_structure
<223> synthetic oligonucleotide used to join DNA fragments with non-cohesive ends.

<400> 13
ttaggcttag gtggcggtgg atccggcggt ggtggatctt tcccaac 47

<210> 14
<211> 48
<212> DNA
<213> Artificial Sequence
<220>
<221> misc_structure
<223> synthetic oligonucleotide used to join DNA fragments with non-cohesive ends.

<400> 14
aattgttggg aaagatccac caccgccgga tccaccgcca cctaagcc 48

<210> 15
<211> 62
<212> DNA
<213> Artificial Sequence
<220>
<221> misc_structure
<223> synthetic oligonucleotide used to join DNA
fragments with non-cohesive ends.

<400> 15
ttaggcttag gcggtggtgg atctggtggc ggcggatctg gtggcggtgg atccttccca 60
ac 62

<210> 16
<211> 63
<212> DNA
<213> Artificial Sequence
<220>
<221> misc_structure
<223> synthetic oligonucleotide used to join DNA
fragments with non-cohesive ends.

<400> 16
aattgttggg aaggatccac cgccaccaga tccgccgcca ccagatccac caccgcctaa 60
gcc 63

<210> 17
<211> 1782
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> (1)..(1755)

<400> 17
gat gca cac aag agt gag gtt gct cat cgg ttt aaa gat ttg gga gaa 48
Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1 5 10 15

gaa aat ttc aaa gcc ttg gtg ttg att gcc ttt gct cag tat ctt cag 96
Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
20 25 30

cag tgt cca ttt gaa gat cat gta aaa tta gtg aat gaa gta act gaa 144
Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
35 40 45

ttt gca aaa aca tgt gtt gct gat gag tca gct gaa aat tgt gac aaa 192
Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
50 55 60

```
tca ctt cat acc ctt ttt gga gac aaa tta tgc aca gtt gca act ctt   240
Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
 65                  70                  75                  80

cgt gaa acc tat ggt gaa atg gct gac tgc tgt gca aaa caa gaa cct   288
Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
                85                  90                  95

gag aga aat gaa tgc ttc ttg caa cac aaa gat gac aac cca aac ctc   336
Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
            100                 105                 110

ccc cga ttg gtg aga cca gag gtt gat gtg atg tgc act gct ttt cat   384
Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
        115                 120                 125

gac aat gaa gag aca ttt ttg aaa aaa tac tta tat gaa att gcc aga   432
Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
    130                 135                 140

aga cat cct tac ttt tat gcc ccg gaa ctc ctt ttc ttt gct aaa agg   480
Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145                 150                 155                 160

tat aaa gct gct ttt aca gaa tgt tgc caa gct gct gat aaa gct gcc   528
Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
                165                 170                 175

tgc ctg ttg cca aag ctc gat gaa ctt cgg gat gaa ggg aag gct tcg   576
Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
            180                 185                 190

tct gcc aaa cag aga ctc aaa tgt gcc agt ctc caa aaa ttt gga gaa   624
Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
        195                 200                 205

aga gct ttc aaa gca tgg gca gtg gct cgc ctg agc cag aga ttt ccc   672
Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
    210                 215                 220

aaa gct gag ttt gca gaa gtt tcc aag tta gtg aca gat ctt acc aaa   720
Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys
225                 230                 235                 240

gtc cac acg gaa tgc tgc cat gga gat ctg ctt gaa tgt gct gat gac   768
Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
                245                 250                 255

agg gcg gac ctt gcc aag tat atc tgt gaa aat cag gat tcg atc tcc   816
Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
            260                 265                 270
```

```
agt aaa ctg aag gaa tgc tgt gaa aaa cct ctg ttg gaa aaa tcc cac   864
Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
        275                 280                 285

tgc att gcc gaa gtg gaa aat gat gag atg cct gct gac ttg cct tca   912
Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
    290                 295                 300

tta gct gct gat ttt gtt gaa agt aag gat gtt tgc aaa aac tat gct   960
Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305                 310                 315                 320

gag gca aag gat gtc ttc ctg ggc atg ttt ttg tat gaa tat gca aga   1008
Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
                325                 330                 335

agg cat cct gat tac tct gtc gtg ctg ctg ctg aga ctt gcc aag aca   1056
Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
            340                 345                 350

tat gaa acc act cta gag aag tgc tgt gcc gct gca gat cct cat gaa   1104
Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
        355                 360                 365

tgc tat gcc aaa gtg ttc gat gaa ttt aaa cct ctt gtg gaa gag cct   1152
Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
    370                 375                 380

cag aat tta atc aaa caa aac tgt gag ctt ttt gag cag ctt gga gag   1200
Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385                 390                 395                 400

tac aaa ttc cag aat gcg cta tta gtt cgt tac acc aag aaa gta ccc   1248
Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
                405                 410                 415

caa gtg tca act cca act ctt gta gag gtc tca aga aac cta gga aaa   1296
Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
            420                 425                 430

gtg ggc agc aaa tgt tgt aaa cat cct gaa gca aaa aga atg ccc tgt   1344
Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
        435                 440                 445

gca gaa gac tat cta tcc gtg gtc ctg aac cag tta tgt gtg ttg cat   1392
Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
    450                 455                 460

gag aaa acg cca gta agt gac aga gtc aca aaa tgc tgc aca gag tcc   1440
Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465                 470                 475                 480
```

```
ttg gtg aac agg cga cca tgc ttt tca gct ctg gaa gtc gat gaa aca  1488
Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
                485                 490                 495

tac gtt ccc aaa gag ttt aat gct gaa aca ttc acc ttc cat gca gat  1536
Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
            500                 505                 510

ata tgc aca ctt tct gag aag gag aga caa atc aag aaa caa act gca  1584
Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
        515                 520                 525

ctt gtt gag ctt gtg aaa cac aag ccc aag gca aca aaa gag caa ctg  1632
Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
    530                 535                 540

aaa gct gtt atg gat gat ttc gca gct ttt gta gag aag tgc tgc aag  1680
Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545                 550                 555                 560

gct gac gat aag gag acc tgc ttt gcc gag gag ggt aaa aaa ctt gtt  1728
Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
                565                 570                 575

gct gca agt caa gct gcc tta ggc tta taacatctac atttaaaagc atctcag 1782
Ala Ala Ser Gln Ala Ala Leu Gly Leu
            580                 585
```

<210> 18
<211> 585
<212> PRT
<213> Homo Sapiens

<400> 18

```
Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
  1               5                  10                  15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
             20                  25                  30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
         35                  40                  45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
     50                  55                  60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
 65                  70                  75                  80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
                 85                  90                  95
```

```
Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
            100                 105                 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
        115                 120                 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
    130                 135                 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145                 150                 155                 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
                165                 170                 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
            180                 185                 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
        195                 200                 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
    210                 215                 220

Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys
225                 230                 235                 240

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
                245                 250                 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
            260                 265                 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
        275                 280                 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
    290                 295                 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305                 310                 315                 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
                325                 330                 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
            340                 345                 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
        355                 360                 365
```


Finnegan, Henderson, Farabow,
Garrett & Dunner, L.L.P.
901 New York Avenue, N.W.
Washington, D.C. 20001-4413

```
Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
    370                 375                 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385                 390                 395                 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
                405                 410                 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
            420                 425                 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
        435                 440                 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
    450                 455                 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465                 470                 475                 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
                485                 490                 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
            500                 505                 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
        515                 520                 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
    530                 535                 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545                 550                 555                 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
                565                 570                 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu
            580                 585

<210> 19
<211> 58
<212> DNA
<213> Artificial Sequence
<220>
<221> primer_bind
<223> primer used to generate XhoI and ClaI site in pPPC0006

<400> 19
gcctcgagaa aagagatgca cacaagagtg aggttgctca tcgatttaaa gatttggg    58
```

<210> 20
<211> 59
<212> DNA
<213> Artificial Sequence
<220>
<221> primer_bind
<223> primer used in generation XhoI and ClaI site in pPPC0006

<400> 20
aatcgatgag caacctcact cttgtgtgca tctcttttct cgaggctcct ggaataagc 59

<210> 21
<211> 24
<212> DNA
<213> Artificial Sequence
<220>
<221> primer_bind
<223> primer used in generation XhoI and ClaI site in pPPC0006

<400> 21
tacaaactta agagtccaat tagc 24

<210> 22
<211> 29
<212> DNA
<213> Artificial Sequence
<220>
<221> primer_bind
<223> primer used in generation XhoI and ClaI site in pPPC0006

<400> 22
cacttctcta gagtggtttc atatgtctt 29

<210> 23
<211> 60
<212> DNA
<213> Artificial Sequence
<220>
<221> Misc_Structure
<223> Synthetic oligonucleotide used to alter restriction sites in pPPC0007

<400> 23
aagctgcctt aggcttataa taaggcgcgc cggccggccg tttaaactaa gcttaattct 60

<210> 24
<211> 60
<212> DNA
<213> Artificial Sequence
<220>
<221> Misc_Structure
<223> Synthetic oligonucleotide used to alter restriction sites in pPPC0007

<400> 24
agaattaagc ttagtttaaa cggccggccg gcgcgcctta ttataagcct aaggcagctt 60

<210> 25
<211> 32
<212> DNA
<213> Artificial Sequence
<220>
<221> primer_bind
<223> forward primer useful for generation of albumin fusion protein in which the albumin moiety is N-terminal of the Therapeutic Protein
<220>
<221> misc feature
<222> (18)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (19)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (20)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (21)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (22)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (23)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (24)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (25)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (26)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (27)
<223> n equals a,t,g, or c
<220>

MAILING ADDRESS OF SENDER

Finnegan, Henderson, Farabow,
Garrett & Dunner, L.L.P.
901 New York Avenue, N.W.
Washington, D.C. 20001-4413

<221> misc feature
<222> (28)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (29)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (30)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (31)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (32)
<223> n equals a,t,g, or c

<400> 25
aagctgcctt aggcttannn nnnnnnnnnn nn 32

<210> 26
<211> 51
<212> DNA
<213> Artificial Sequence
<220>
<221> primer_bind
<223> reverse primer useful for generation of albumin fusion protein in which the albumin moiety is N-terminal of the Therapeutic Protein
<220>
<221> misc feature
<222> (37)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (38)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (39)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (40)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (41)
<223> n equals a,t,g, or c
<220>

<221> misc feature
<222> (42)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (43)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (44)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (45)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (46)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (47)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (48)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (49)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (50)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (51)
<223> n equals a,t,g, or c

<400> 26
gcgcgcgttt aaacggccgg ccggcgcgcc ttattannnn nnnnnnnnnn n 51

<210> 27
<211> 33
<212> DNA
<213> Artificial Sequence
<220>
<223> forward primer useful for generation of albumin fusion protein in which the albumin moiety is c-terminal of the Therapeutic Protein
<220>
<221> misc feature

<222> (19)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (20)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (21)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (22)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (23)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (24)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (25)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (26)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (27)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (28)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (29)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (30)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (31)
<223> n equals a,t,g, or c
<220>
<221> misc feature

<222> (32)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (33)
<223> n equals a,t,g, or c

<400> 27
aggagcgtcg acaaaagann nnnnnnnnnn nnn 33

<210> 28
<211> 52
<212> DNA
<213> Artificial Sequence
<220>
<221> primer_bind
<223> reverse primer useful for generation of albumin fusion protein in which the albumin moiety is c-terminal of the Therapeutic Protein
<220>
<221> misc feature
<222> (38)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (39)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (40)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (41)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (42)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (43)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (44)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (45)
<223> n equals a,t,g, or c
<220>
<221> misc feature

<222> (46)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (47)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (48)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (49)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (50)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (51)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (52)
<223> n equals a,t,g, or c

<400> 28
ctttaaatcg atgagcaacc tcactcttgt gtgcatcnnn nnnnnnnnnn nn 52

<210> 29
<211> 24
<212> PRT
<213> Artificial Sequence
<220>
<221> signal
<223> signal peptide of natural human serum albumin protein

<400> 29
Met Lys Trp Val Ser Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
1 5 10 15

Tyr Ser Arg Ser Leu Asp Lys Arg
20

<210> 30
<211> 114
<212> DNA
<213> Artificial Sequence
<220>
<221> primer_bind
<223> forward primer useful for generation of PC4:HSA albumin fusion VECTOR

<220>
<221> misc_feature
<222> (5)..(10)
<223> BamHI retsriction site
<220>
<221> misc_feature
<222> (11)..(16)
<223> Hind III retsriction site
<220>
<221> misc_feature
<222> (17)..(27)
<223> Kozak sequence
<220>
<221> misc_feature
<222> (25)..(97)
<223> cds natural signal sequence of human serum albumin
<220>
<221> misc_feature
<222> (75)..(81)
<223> XhoI restriction site
<220>
<221> misc_feature
<222> (98)..(114)
<223> cds first six amino acids of human serum albumin

<400> 30
tcagggatcc aagcttccgc caccatgaag tgggtaacct ttatttccct tctttttctc 60

tttagctcgg cttactcgag gggtgtgttt cgtcgagatg cacacaagag tgag 114

<210> 31
<211> 43
<212> DNA
<213> Artificial Sequence
<220>
<221> primer_bind
<223> reverse primer useful for generation of PC4:HSA albumin fusion VECTOR
<220>
<221> misc_feature
<222> (6)..(11)
<223> Asp718 restriction site
<220>
<221> misc_feature
<222> (12)..(17)
<223> EcoRI restriction site
<220>
<221> misc_feature
<222> (15)..(17)
<223> reverse complement of stop codon
<220>
<221> misc_feature
<222> (18)..(25)

<223> AscI restriction site
<220>
<221> misc_feature
<222> (18)..(43)
<223> reverse complement of DNA sequence encoding last 9 amino acids

<400> 31
gcagcggtac cgaattcggc gcgccttata agcctaaggc agc 43

<210> 32
<211> 46
<212> DNA
<213> Artificial Sequence
<220>
<221> primer_bind
<223> forward primer useful for inserting Therapeutic protein into pC4:HSA vector
<220>
<221> misc feature
<222> (29)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (30)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (31)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (32)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (33)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (34)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (35)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (36)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (37)

Finnegan, Henderson, Farabow,
Garrett & Dunner, L.L.P.
901 New York Avenue, N.W.
Washington, D.C. 20001-4413

<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (38)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (39)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (40)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (41)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (42)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (43)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (44)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (45)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (46)
<223> n equals a,t,g, or c

<400> 32
ccgccgctcg aggggtgtgt ttcgtcgann nnnnnnnnnn nnnnnn 46

<210> 33
<211> 55
<212> DNA
<213> Artificial Sequence
<220>
<221> primer_bind
<223> reverse primer useful for inserting Therapeutic protein into pC4:HSA vector
<220>
<221> misc feature
<222> (38)

<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (39)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (40)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (41)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (42)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (43)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (44)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (45)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (46)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (47)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (48)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (49)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (50)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (51)

Finnegan, Henderson, Farabow,
Garrett & Dunner, L.L.P.
901 New York Avenue, N.W.
Washington, D.C. 20001-4413

<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (52)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (53)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (54)
<223> n equals a,t,g, or c
<220>
<221> misc feature
<222> (55)
<223> n equals a,t,g, or c

<400> 33
agtcccatcg atgagcaacc tcactcttgt gtgcatcnnn nnnnnnnnnn nnnnn 55

<210> 34
<211> 17
<212> PRT
<213> Artificial Sequence
<220>
<221> signal
<223> Stanniocalcin signal peptide

<400> 34
Met Leu Gln Asn Ser Ala Val Leu Leu Leu Val Ile Ser Ala Ser Ala
1 5 10 15

<210> 35
<211> 22
<212> PRT
<213> Artificial Sequence
<220>
<221> signal
<223> Synthetic signal peptide

<400> 35
Met Pro Thr Trp Ala Trp Trp Leu Phe Leu Val Leu Leu Leu Ala Leu
1 5 10 15

Trp Ala Pro Ala Arg Gly
20

<210> 36
<211> 23
<212> DNA
<213> Artificial Sequence
<220>

<221>primer_bind
<223>Degenerate VH forward primer useful for amplifying human VH domains

<400> 36
caggtgcagc tggtgcagtc tgg 23

<210> 37
<211> 23
<212> DNA
<213> Artificial Sequence
<220>
<221>primer_bind
<223>Degenerate VH forward primer useful for amplifying human VH domains

<400> 37
caggtcaact taagggagtc tgg 23

<210> 38
<211> 23
<212> DNA
<213> Artificial Sequence
<220>
<221>primer_bind
<223>Degenerate VH forward primer useful for amplifying human VH domains

<400> 38
gaggtgcagc tggtggagtc tgg 23

<210> 39
<211> 23
<212> DNA
<213> Artificial Sequence
<220>
<221>primer_bind
<223>Degenerate VH forward primer useful for amplifying human VH domains

<400> 39
caggtgcagc tgcaggagtc ggg 23

<210> 40
<211> 23
<212> DNA
<213> Artificial Sequence
<220>
<221>primer_bind
<223>Degenerate VH forward primer useful for amplifying human VH domains

<400> 40
gaggtgcagc tgttgcagtc tgc 23

<210> 41
<211> 23

<212> DNA
<213> Artificial Sequence
<220>
<221>primer_bind
<223>Degenerate VH forward primer useful for amplifying human VH domains

<400> 41
caggtacagc tgcagcagtc agg 23

<210> 42
<211> 24
<212> DNA
<213> Artificial Sequence
<220>
<221>primer_bind
<223>Degenerate JH reverse primer useful for amplifying human VH domains

<400> 42
tgaggagacg gtgaccaggg tgcc 24

<210> 43
<211> 24
<212> DNA
<213> Artificial Sequence
<220>
<221>primer_bind
<223>Degenerate JH reverse primer useful for amplifying human VH domains

<400> 43
tgaagagacg gtgaccattg tccc 24

<210> 44
<211> 24
<212> DNA
<213> Artificial Sequence
<220>
<221>primer_bind
<223>Degenerate JH reverse primer useful for amplifying human VH domains

<400> 44
tgaggagacg gtgaccaggg ttcc 24

<210> 45
<211> 24
<212> DNA
<213> Artificial Sequence
<220>
<221>primer_bind
<223>Degenerate JH reverse primer useful for amplifying human VH domains

<400> 45
tgaggagacg gtgaccgtgg tccc 24

<210> 46
<211> 23
<212> DNA
<213> Artificial Sequence
<220>
<221>primer_bind
<223>Degenerate Vkappa forward primer useful for amplifying human VL domains

<400> 46
gacatccaga tgacccagtc tcc 23

<210> 47
<211> 23
<212> DNA
<213> Artificial Sequence
<220>
<221>primer_bind
<223>Degenerate Vkappa forward primer useful for amplifying human VL domains

<400> 47
gatgttgtga tgactcagtc tcc 23

<210> 48
<211> 23
<212> DNA
<213> Artificial Sequence
<220>
<221>primer_bind
<223>Degenerate Vkappa forward primer useful for amplifying human VL domains

<400> 48
gatattgtga tgactcagtc tcc 23

<210> 49
<211> 23
<212> DNA
<213> Artificial Sequence
<220>
<221>primer_bind
<223>Degenerate Vkappa forward primer useful for amplifying human VL domains

<400> 49
gaaattgtgt tgacgcagtc tcc 23

<210> 50
<211> 23
<212> DNA
<213> Artificial Sequence
<220>
<221>primer_bind
<223>Degenerate Vkappa forward primer useful for amplifying human VL domains

<400> 50
gacatcgtga tgacccagtc tcc 23

<210> 51
<211> 23
<212> DNA
<213> Artificial Sequence
<220>
<221>primer_bind
<223>Degenerate Vkappa forward primer useful for amplifying human VL domains

<400> 51
gaaacgacac tcacgcagtc tcc 23

<210> 52
<211> 23
<212> DNA
<213> Artificial Sequence
<220>
<221>primer_bind
<223>Degenerate Vkappa forward primer useful for amplifying human VL domains

<400> 52
gaaattgtgc tgactcagtc tcc 23

<210> 53
<211> 23
<212> DNA
<213> Artificial Sequence
<220>
<221>primer_bind
<223>Degenerate Vlambda forward primer useful for amplifying human VL domains

<400> 53
cagtctgtgt tgacgcagcc gcc 23

<210> 54
<211> 23
<212> DNA
<213> Artificial Sequence
<220>
<221>primer_bind
<223>Degenerate Vlambda forward primer useful for amplifying human VL domains

<400> 54
cagtctgccc tgactcagcc tgc 23

<210> 55
<211> 23
<212> DNA
<213> Artificial Sequence
<220>

<221>primer_bind
<223>Degenerate Vlambda forward primer useful for amplifying human VL domains

<400> 55
tcctatgtgc tgactcagcc acc 23

<210> 56
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate Vlambda forward primer useful for amplifying human VL domains

<400> 56
tcttctgagc tgactcagga ccc 23

<210> 57
<211> 23
<212> DNA
<213> Artificial Sequence
<220>
<221>primer_bind
<223>Degenerate Vlambda forward primer useful for amplifying human VL domains

<400> 57
cacgttatac tgactcaacc gcc 23

<210> 58
<211> 23
<212> DNA
<213> Artificial Sequence
<220>
<221>primer_bind
<223>Degenerate Vlambda forward primer useful for amplifying human VL domains

<400> 58
caggctgtgc tcactcagcc gtc 23

<210> 59
<211> 23
<212> DNA
<213> Artificial Sequence
<220>
<221>primer_bind
<223>Degenerate Vlambda forward primer useful for amplifying human VL domains

<400> 59
aattttatgc tgactcagcc cca 23

<210> 60
<211> 24
<212> DNA
<213> Artificial Sequence
<220>
<221>primer_bind
<223>Degenerate Jkappa reverse primer useful for amplifying human VL domains

<400> 60
acgtttgatt tccaccttgg tccc 24

<210> 61
<211> 24
<212> DNA
<213> Artificial Sequence
<220>
<221>primer_bind
<223>Degenerate Jkappa reverse primer useful for amplifying human VL domains

<400> 61
acgtttgatc tccagcttgg tccc 24

<210> 62
<211> 24
<212> DNA
<213> Artificial Sequence
<220>
<221>primer_bind
<223>Degenerate Jkappa reverse primer useful for amplifying human VL domains

<400> 62
acgtttgata tccactttgg tccc 24

<210> 63
<211> 24
<212> DNA
<213> Artificial Sequence
<220>
<221>primer_bind
<223>Degenerate Jkappa reverse primer useful for amplifying human VL domains

<400> 63
acgtttgatc tccaccttgg tccc 24

<210> 64
<211> 24
<212> DNA
<213> Artificial Sequence
<220>
<221>primer_bind
<223>Degenerate Jkappa reverse primer useful for amplifying human VL domains

<400> 64
acgtttaatc tccagtcgtg tccc 24

<210> 65
<211> 23
<212> DNA
<213> Artificial Sequence
<220>
<221>primer_bind
<223>Degenerate Jlambda reverse primer useful for amplifying human VL domains

<400> 65
cagtctgtgt tgacgcagcc gcc 23

<210> 66
<211> 23
<212> DNA
<213> Artificial Sequence
<220>
<221>primer_bind
<223>Degenerate Jlambda reverse primer useful for amplifying human VL domains

<400> 66
cagtctgccc tgactcagcc tgc 23

<210> 67
<211> 23
<212> DNA
<213> Artificial Sequence
<220>
<221>primer_bind
<223>Degenerate Jlambda reverse primer useful for amplifying human VL domains

<400> 67
tcctatgtgc tgactcagcc acc 23

<210> 68
<211> 23
<212> DNA
<213> Artificial Sequence
<220>
<221>primer_bind
<223>Degenerate Jlambda reverse primer useful for amplifying human VL domains

<400> 68
tcttctgagc tgactcagga ccc 23

<210> 69
<211> 23
<212> DNA
<213> Artificial Sequence
<220>

<221>primer_bind
<223>Degenerate Jlambda reverse primer useful for amplifying human VL domains

<400> 69
cacgttatac tgactcaacc gcc 23

<210> 70
<211> 23
<212> DNA
<213> Artificial Sequence
<220>
<221>primer_bind
<223>Degenerate Jlambda reverse primer useful for amplifying human VL domains

<400> 70
caggctgtgc tcactcagcc gtc 23

<210> 71
<211> 23
<212> DNA
<213> Artificial Sequence
<220>
<221>primer_bind
<223>Degenerate Jlambda reverse primer useful for amplifying human VL domains

<400> 71
aattttatgc tgactcagcc cca 23

<210> 72
<211> 15
<212> PRT
<213> Artificial Sequence
<220>
<221>turn
<223>Linker peptide that may be used to join VH and VL domains in an scFv.

<400> 72
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 73
<211> 733
<212> DNA
<213> Homo sapiens

<400> 73
gggatccgga gcccaaatct tctgacaaaa ctcacacatg cccaccgtgc ccagcacctg 60

aattcgaggg tgcaccgtca gtcttcctct tccccccaaa acccaaggac accctcatga 120

tctcccggac tcctgaggtc acatgcgtgg tggtggacgt aagccacgaa gaccctgagg 180

tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca aagccgcggg 240

aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg caccaggact 300

ggctgaatgg caaggagtac aagtgcaagg tctccaacaa agccctccca acccccatcg 360

agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac accctgcccc 420

catcccggga tgagctgacc aagaaccagg tcagcctgac ctgcctggtc aaaggcttct 480

atccaagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac aactacaaga 540

ccacgcctcc cgtgctggac tccgacggct ccttcttcct ctacagcaag ctcaccgtgg 600

acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat gaggctctgc 660

acaaccacta cacgcagaag agcctctccc tgtctccggg taaatgagtg cgacggccgc 720

gactctagag gat 733

<210> 74
<211> 5
<212> PRT
<213> Artificial sequence
<220>
<221> misc_structure
<223> membrane proximal motif of class 1 cytokine receptors
<220>
<221> misc_feature
<222> (3)
<223> Xaa equals any

<400> 74
Trp Ser Xaa Trp Ser
1 5

<210> 75
<211> 86
<212> DNA
<213> Artificial Sequence
<220>
<221> primer_bind
<223> forward primer useful for generation of a synthetic gamma activation site (GAS) containing promoter element

<400> 75
gcgcctcgag atttccccga aatctagatt tccccgaaat gatttccccg aaatgatttc 60

cccgaaatat ctgccatctc aattag 86

<210> 76
<211> 27

<212> DNA
<213> Artificial Sequence
<220>
<221> primer_bind
<223> reverse primer useful for generation of a synthetic gamma activation site (GAS) containing promoter element

<400> 76
gcggcaagct ttttgcaaag cctaggc 27

<210> 77
<211> 271
<212> DNA
<213> Artificial Sequence
<220>
<221> misc_feature
<223> Synthetic GAS-SV40 promoter sequence

<400> 77
ctcgagattt ccccgaaatc tagatttccc cgaaatgatt tccccgaaat gatttccccg 60

aaatatctgc catctcaatt agtcagcaac catagtcccg cccctaactc cgcccatccc 120

gcccctaact ccgcccagtt ccgcccattc tccgccccat ggctgactaa ttttttttat 180

ttatgcagag gccgaggccg cctcggcctc tgagctattc cagaagtagt gaggaggctt 240

ttttggaggc ctaggctttt gcaaaaagct t 271

<210> 78
<211> 32
<212> DNA
<213> Artificial Sequence
<220>
<221> primer_bind
<223> primer useful for generation of a EGR/SEAP reporter construct

<400> 78
gcgctcgagg gatgacagcg atagaacccc gg 32

<210> 79
<211> 31
<212> DNA
<213> Artificial Sequence
<220>
<221> primer_bind
<223> primer useful for generation of a EGR/SEAP reporter construct

<400> 79
gcgaagcttc gcgactcccc ggatccgcct c 31

<210> 80
<211> 12
<212> DNA
<213> Artificial Sequence
<220>
<221> misc_binding
<223> NF-KB binding site

<400> 80
ggggactttc cc 12

<210> 81
<211> 73
<212> DNA
<213> Artificial Sequence
<220>
<221> primer_bind
<223> forward primer useful for generation of a vector containing the NF-KB promoter element

<400> 81
gcggcctcga ggggactttc ccggggactt tccggggact ttccgggact ttccatcctg 60

ccatctcaat tag 73

<210> 82
<211> 256
<212> DNA
<213> Artificial Sequence
<220>
<221> misc_feature
<223> Synthetic NF-KB/SV40 promoter

<400> 82
ctcgagggga ctttcccggg gactttccgg ggactttccg ggactttcca tctgccatct 60

caattagtca gcaaccatag tcccgccccc aactccgccc atcccgcccc taactccgcc 120

cagttccgcc cattctccgc cccatggctg actaattttt tttatttatg cagaggccga 180

ggccgcctcg gcctctgagc tattccagaa gtagtgagga ggcttttttg gaggcctagg 240

cttttgcaaa aagctt 256